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SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

JAPAN AS REPRESENTED BY THE PRESIDENT OF THE UNIVERSITY OF TOKYO

<120> METHOD FOR DIAGNOSING COLORECTAL CANCERS

<130> ONC-X0309P

<160> 23

<170> PatentIn version 3.1

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<213> Homo sapiens

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<222> (294)..(1688)

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gctctgataa cagtcctttt ccctggcgct cacttcgtgc ctggcaccgc gctgggcgc      240
tcaagaccgt tgtctcttcg atcgcttctt tggacttggc gaccatttca gag atg      296
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Met

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Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys	
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cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa	392
Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu	
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att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga	440
Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly	
35 40 45	
aag ctg act gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc	488
Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val	
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ctt gag gct gag aag gag aag aat gct tat caa ctc aca gag aag gac	536
Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp	
70 75 80	
aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act	584
Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr	
85 90 95	
acc gca ttg ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg	632
Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg	
100 105 110	
agg gag cag gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa	680
Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys	

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caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa			728
Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys			
130	135	140	145
acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac			776
Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn			
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tca tca ata aat aat att cat gaa atg gaa ata cag ctg aaa gat gct			824
Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala			
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ctg gag aaa aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc			872
Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val			
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Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr			
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Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser			
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Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu			
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245 250 255	
ctg agt ttt gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa	1112
Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln	
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Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala	
275 280 285	
gat gtg caa cat ctg gaa gat gat agg cat aaa aca gag aag ata caa	1208
Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln	
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aaa ctc agg gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag	1256
Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu	
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aag aag aga tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca	1304
Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr	
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Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu	
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caa cag atg cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac	1400
Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp	
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 Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu Arg
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aaa gca aga aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat 1496
 Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His
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 Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu
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act gag cat cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag 1688
 Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
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<213> Homo sapiens

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Lys Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly
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Glu Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys
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Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
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Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys

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Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu			
	100	105	110
Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu			
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Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser			
	130	135	140
Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe			
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Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp			
	165	170	175
Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu			
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Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys			
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	210	215	220
Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu			
225	230	235	240

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Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr

245

250

255

Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr

260

265

270

Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg

275

280

285

Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile

290

295

300

Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu

305

310

315

320

Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr

325

330

335

Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu

340

345

350

Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu

355

360

365

Asp Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu

370

375

380

Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu

385

390

395

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His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr

405

410

415

Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala

420

425

430

Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro

435

440

445

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450

455

460

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10/20

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11/20

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1 2 / 2 0

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22

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1 3 / 2 0

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1 4 / 2 0

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siRNA

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<222> (489)..(492)

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